Amendments to the Claims

Claim 1 (Currently Amended): A method for determining the prognosis of a patient with breast cancer, the method comprising assigning a prognosis to the patient based on the ~~expression~~ levels of nucleic acid expression products ~~in a breast tumour of said patient~~ of a prognostic set of genes in a breast tumour of said patient, wherein the prognostic set includes adenine phosphoribosyltransferase, MCM4 minichromosome ~~maintainance~~ maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727, and wherein a patient having higher levels of nucleic acid expression products of adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727 has a poorer prognosis, said method optionally comprising the step of determining as least one status selected from the group consisting of estrogen receptor (ER) status and Erb2 status of the tumour sample.

Claim 2 (Currently Amended): The [[A]] method ~~according to~~ of claim 1, wherein the prognostic set comprises at least 10, 20, 30, 40, 50, 60 or all of the genes of Table S6.

Claim 3 (Cancelled)

Claim 4 (Cancelled)

Claim 5 (Currently Amended): The [[A]] method ~~according to~~ of claim 1 comprising the steps of:

(a) obtaining a breast tumour sample from the patient; and

(b) measuring the ~~expression~~ levels of said nucleic acid expression products in the sample of the genes of the prognostic set.

Claim 6 (Currently Amended): The [[A]] method ~~according to~~ of claim 5 wherein step (b) comprises contacting said nucleic acid expression products obtained from the sample with a plurality of binding members capable of binding to said nucleic acid expression products ~~that are indicative of the expression of genes of the prognostic set~~, wherein such binding may be measured.

Claim 7 (Currently Amended): The [[A]] method ~~according to~~ of claim 6 wherein the binding members are complementary nucleic acid sequences ~~or specific antibodies~~.

Claim 8 (Currently Amended): The [[A]] method ~~according to~~ of claim 1, comprising classifying the sample of breast tumour as being of either high Nottingham Prognostic Index (NPI) or low NPI, or as either of good or bad prognosis, wherein an upregulation of the nucleic acid expression products of adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727 is indicative of a poor prognosis or high NPI, and wherein a downregulation of the nucleic acid expression products of adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727 is indicative of a good prognosis or low NPI.

Claim 9 (Currently Amended): The [[A]] method ~~according to~~ of claim 1, wherein the step of assigning a prognosis is carried out by comparing the expression profile from the breast tumour sample under test with previously obtained profiles and/or a previously determined standard profile which is characteristic of a particular prognosis.

Claim 10 (Currently Amended): The [[A]] method ~~according to~~ of claim 9 wherein the previously obtained profiles are stored as

a database of profiles.

Claim 11 (Currently Amended): The [[A]] method ~~according to~~ of claim 1 further comprising comparing the expression levels of the prognostic set in the breast tumour sample before and after treatment to detect a change in the expression profile indicative of an improved prognosis or worsened prognosis.

Claim 12 (Currently Amended): An apparatus ~~Apparatus~~ for assigning a prognosis to a breast tumour sample, which apparatus comprises a solid support to which are attached a plurality of nucleic acid binding members, each binding member being capable of specifically and independently binding to an expression product of one of a prognostic set of genes, wherein the prognostic set includes adenine phosphoribosyltransferase, MCM4 minichromosome ~~maintainance~~ maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727, and wherein said solid support houses nucleic acid binding members for not more than 500 different genes.

Claim 13 (Currently Amended): The apparatus ~~Apparatus according to~~ of claim 12, wherein the prognostic set comprises at least 5, 10, 20, 30, 40, 50, 60 or all of the genes of Table S6.

Claim 14 (Currently Amended): The apparatus ~~Apparatus according to~~ of claim 12 wherein the solid support has attached thereto only binding members that are capable of specifically and independently binding to expression products of the genes identified in Table S6.

Claim 15 (Cancelled)

Claim 16 (Currently Amended): A kit for assigning a prognosis to a patient with breast cancer, said kit comprising a

plurality of nucleic acid binding members capable of specifically binding to nucleic acid expression products of genes of a prognostic set of genes and a detection reagent, wherein the prognostic set includes adenine phosphoribosyltransferase, MCM4 minichromosome ~~maintainance~~ maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727, wherein said kit optionally ~~comprising~~ comprises the apparatus of claim 12.

Claim 17 (Currently Amended): The [[A]] kit ~~according to~~ of claim 16, wherein the prognostic set comprises at least 10, 20, 30, 40, 50, 60 or all of the genes of Table S6.

Claim 18 (Currently Amended): The [[A]] kit ~~according to~~ of claim 16, further comprising a data analysis tool, wherein the data analysis tool is a computer program.

Claim 19 (Currently Amended): The [[A]] kit ~~according to~~ of claim 18 wherein the data analysis tool comprises an algorithm adapted to discriminate between the expression profiles of tumours with differing prognoses.

Claim 20 (Currently Amended): The [[A]] kit ~~according to~~ of claim 16 comprising expression profiles from breast tumour samples with known prognoses and/or expression profiles characteristic of a particular prognosis.

Claim 21 (Cancelled)

Claim 22 (Currently Amended): A kit ~~according to claims 16 comprising~~ for assigning a prognosis to a patient with breast cancer, said kit comprising a plurality of nucleic acid binding members capable of specifically binding to nucleic acid expression products of genes of a prognostic set of genes and a detection reagent, wherein the prognostic set includes

adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727, wherein said binding members are nucleotide primers capable of binding to the nucleic acid expression products of the genes of the prognostic set such that ~~they~~ the nucleic acid expression products can be amplified by ~~in a~~ PCR.

Claim 23 (Currently Amended): A method of producing a nucleic acid expression profile for a breast tumour sample comprising the steps of

(a) isolating nucleic acid expression products from said breast tumour sample;

(b) identifying the expression levels of nucleic acid expression products of a prognostic set of genes, wherein the prognostic set of genes comprises adenine phosphoribosyltransferase, MCM4 minichromosome ~~maintainance~~ maintenance deficient 4 (S. cervisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727; and

(c) producing from the expression levels an expression profile for said breast tumour sample.

Claim 24 (Currently Amended): The [[A]] method ~~according to~~ of claim 23, wherein the prognostic set comprises at least 10, 20, 30, 40, 50, 60 or all of the genes of Table S6.

Claim 25 (Currently Amended): The [[A]] method ~~according to~~ of claim 23 comprising adding the expression profile to a gene expression profile database.

Claim 26 (Currently Amended): The [[A]] method ~~according to~~ of claim 23 further comprising comparing the expression profile with a second expression profile or a plurality of second expression profiles characteristic of a particular prognosis.

Claim 27 (Currently Amended): The [[A]] method ~~according to~~ of

claim 26, comprising the steps of:

(a) isolating nucleic acid expression products from a first breast tumour sample; contacting said expression products with a plurality of binding members capable of specifically and independently binding to expression products of the prognostic set; and creating a first expression profile from the expression levels of the prognostic set in the tumour sample;

(b) isolating nucleic acid expression products from a second breast tumour sample of known prognosis; contacting said expression products with a plurality of binding members capable of specifically and independently binding to expression products of the prognostic set of step (a), so as to create a comparable second expression profile of a breast tumour sample; and

(c) comparing the first and second expression profiles to determine the prognosis of the first breast tumour sample, wherein a match of said first and second expression profiles indicates said known prognosis.

Claims 28-37 (Cancelled)